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EXAMINER	
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ART UNIT	**PAPER NUMBER**
1643	

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Please find below and/or attached an Office communication concerning this application or proceeding.

Office Action Summary	Application No.	Applicant(s)	
	10/764,390	RAITANO ET AL.	
	Examiner	Art Unit	
	Karen A. Canella	1643	

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --

Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE 3 MONTH(S) OR THIRTY (30) DAYS, WHICHEVER IS LONGER, FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133). Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

Status

1)☐ Responsive to communication(s) filed on _____.

2a)☐ This action is **FINAL**. 2b)☒ This action is non-final.

3)☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

Disposition of Claims

4)☐ Claim(s) 49-78 is/are pending in the application.

4a) Of the above claim(s) _____ is/are withdrawn from consideration.

5)☐ Claim(s) _____ is/are allowed.

6)☐ Claim(s) 49-78 is/are rejected.

7)☐ Claim(s) _____ is/are objected to.

8)☐ Claim(s) _____ are subject to restriction and/or election requirement.

Application Papers

9)☐ The specification is objected to by the Examiner.

10)☐ The drawing(s) filed on _____ is/are: a)☐ accepted or b)☐ objected to by the Examiner.

Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).

Replacement drawing sheet(s) including the correction is required if the drawing(s) is objected to. See 37 CFR 1.121(d).

11)☐ The oath or declaration is objected to by the Examiner. Note the attached Office Action or form PTO-152.

Priority under 35 U.S.C. § 119

12)☐ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).

a)☐ All b)☐ Some * c)☐ None of:

1.☐ Certified copies of the priority documents have been received.

2.☐ Certified copies of the priority documents have been received in Application No. _____.

3.☐ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

* See the attached detailed Office action for a list of the certified copies not received.

Attachment(s)

1) ☒ Notice of References Cited (PTO-892)
2) ☐ Notice of Draftsperson's Patent Drawing Review (PTO-948)
3) ☒ Information Disclosure Statement(s) (PTO-1449 or PTO/SB/08) Paper No(s)/Mail Date *April 26, 2005*.
4) ☐ Interview Summary (PTO-413) Paper No(s)/Mail Date. _____.
5) ☐ Notice of Informal Patent Application (PTO-152)
6) ☒ Other: *See Continuation Sheet*.

DETAILED ACTION

1. Acknowledgement is made of applicants election of the Species of SEQ ID NO:3 with traverse. The traversal is on the grounds that SEQ ID NO:3, 5, 7 and 11 are closely related in sequence as indicated by Figure 11. This has been considered and found persuasive. Claims drawn to SEQ ID NO:3, 5, 7 and 11 will be examined together at this time. Claims 49-78 are pending and examined on the merits.

Specification

2. The disclosure and claims are objected to for failing to comply with the Sequence Rules and for duplication of subject matter.

The specification indicates that SEQ ID NO:3 is v.1; SEQ ID NO:5 is v.2; SEQ ID NO:11 is v.5 and SEQ ID NO:7 is v.3. Figure 11 describes v.1 as having a "P" at residue 142 and a "S" at residue 157. Both the Sequence Listing and the CRF indicate that v.1 (SEQ ID NO:3) has an "X" as residues 142, 157 and 612. Figure 11 describes v.2 (SEQ ID NO:5) as differing from v.1 (SEQ ID NO:3) only at residue 157, however v.2 (SEQ ID NO:5) differs from v.1 (SEQ ID NO:3) also at residues 142 and 613 where v.2 has a "P" and a "V" respectively. Figure 11 describes v.5 (SEQ ID NO:11) as differing from v.1 (SEQ ID NO:3) only at residue 142, however, v.5 has a "S" residue at 157 and a "V" residue at 612. Figure 11 describes v.3 (SEQ ID NO:7) as differing from v.1 (SEQ ID NO:3) only in the truncation of the first twenty residues of SEQ ID NO:3 and the addition of 10 extraneous amino acids at the amino terminus, however, v.3 (SEQ ID NO:7) has "P", "S" and "V" at residues 142, 157 and 612, respectively, where v.1 (SEQ ID NO:3) has "X". Thus, the Sequence Listing and CRF fail to reflect the sequences disclosed in the specification.

Further, the specification and the claims incorporate duplicate subject matter. The Sequence Listing and the CRF present SEQ ID NO:5, 9 and 12 which are identical, each having 1072 amino acids and "P", "A" and "V" at residues 142, 157 and 612, respectively. Further, the Sequence Listing and the CRF present SEQ ID NO:7 and 10 to be identical, each having 1063 amino acids and residues "P", "S" and "V" at positions 133, 148 and 603, respectively.

3. The disclosure is objected to because it contains an embedded hyperlink and/or other form of browser-executable code. Applicant is required to delete the embedded hyperlink and/or other form of browser-executable code. Applicant is advised to check the specification carefully for embedded hyperlinks. See MPEP § 608.01.

Claim Objections

4. Claims 61 and 64 are objected to because of the following informalities:

Claim 61 and 64 are objected to for typographical errors. Claim 61 is missing the word "response" before the word comprises' claim 64 has a typographical error in the second occurrence of polynucleotide.

Appropriate correction is required.

Claim Rejections - 35 USC § 101

5. 35 U.S.C. 101 reads as follows:

> Whoever invents or discovers any new and useful process, machine, manufacture, or composition of matter, or any new and useful improvement thereof, may obtain a patent therefor, subject to the conditions and requirements of this title.

6. Claim 72 is rejected under 35 U.S.C. 101 because the claimed invention is directed to non-statutory subject matter.

Claim 72 is rejected under 35 USC §101 because the claimed invention is directed to non-statutory subject matter. The specification teaches that the polynucleotide of the invention be used in gene therapy methods. Thus, when given the broadest reasonable interpretation, a host cell includes a cell in a human being who has undergone gene therapy. The scope of the claim, therefore, encompasses a human being, which is non-statutory subject matter. As such, the recitation of the limitation "isolated host cell" would be remedial. See 1077 O.G. 24, April 21, 1987.

Claim Rejections - 35 USC § 112

7. The following is a quotation of the second paragraph of 35 U.S.C. 112:

The specification shall conclude with one or more claims particularly pointing out and distinctly claiming the subject matter which the applicant regards as his invention.

8. Claims 49-78 are rejected under 35 U.S.C. 112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter which applicant regards as the invention.

(A)Claim 49 is vague and indefinite in the recitation of inducing a specific antibody response. It is unclear if the claim the polypeptides of SEQ ID NO:3, 5, 7 or 11 to be the object of the specific antibody response, or if the variants of SEQ ID NO:3, 5, 7 or 11 can also be the object of the antibody response. Further it is unclear if the "specific antibody response" requires that the antibody bind to one of SEQ ID NO:5 to the exclusion of, for example, SEQ ID NO:7, or if the "specific antibody response" refers to the induction of the IgG response after the initial induction of the IgM response in vivo.

(B)It is unclear how the recitation of "encoded by a nucleotide sequence of SEQ ID NO:2, 3 or 6" encompasses alternate subject matter from polypeptide of SEQ ID NO:3, 5, 7 or 11, because the polypeptide sequence is fixed by the polynucleotide sequence. Thus, as the polypeptide sequences of SEQ ID NO:3, 5, 7 and 11 can be encoded by a multitude of polynucleotide sequences due to degenerate codons, the polynucleotide of SEQ ID NO:2, 3 and 6 can only encode one polypeptide each. Thus the additional text of "encoded by a nucleotide sequence" in claims 49 and 53 appears to be redundant.

(C)Claim 49 recites a polypeptide of SEQ ID NO:3, 5, 7 or 11, or a fragment or variant thereof. It is unclear if "variant thereof' applies to the fragment or to the polypeptide and the fragment. For purpose of examination, "variant thereof' will be applied to both the polypeptide and the fragment.

(D)Claim 54 recites "polypeptide of claim 49 consisting of at least nine contiguous amino acid of the polypeptide". Claim 49 specifies a polypeptide of SEQ ID NO:3, 5, 7 or 11 or a fragment or a variant thereof. The limitation of claim 54 appears to apply to a fragment length rather than the polypeptide thereof, however, claim 54 states the "polypeptide of claim 49" rather than a fragment of claim 49. Further, the recitation of "consisting of at least" is confusing, "consisting of' being closed language and "at least" being open ended language.

(E)Claims 56 and 68 are vague and indefinite for dependent on a table in the specification. The M.P.E.P. (2173.05(s))states

Where possible, claims are to be complete in themselves. Incorporation by reference to a specific figure or table "is permitted only in exceptional circumstances where there is no practical way to define the invention in words and where it is more concise to incorporate by reference than duplicating a drawing or table into the claim. Incorporation by reference is a necessity doctrine, not for applicant's convenience." Ex parte Fressola, 27 USPQ2d 1608, 1609 (Bd. Pat. App. & Inter. 1993) (citations omitted).

(F)Claim 69 recites "the polynucleotide of claim 57", however, claim 57 is drawn to an immunogenic composition comprising a polypeptide.

(G)Claim 73 recites "the cell of claim 66", however, claim 66 is drawn to a polynucleotide, not a cell.

(H)Claim 73 is vague and indefinite in the recitation of "the polypeptide" without further qualification. It is noted that the culturing of host cells produces polypeptides endogenous to the specific host cells which are not related to a recombinant expression product.

(I)The recitation of "first polynucleotide" and "second polynucleotide" in claim 74 lacks proper antecedent basis in claim 63.

(J)Claim 67 is vague and indefinite because it is unclear if the polynucleotide consisting of at least 25 contiguous nucleic acids of the polynucleotide is referring to the polynucleotide encoding the fragments of claim 49, or if claim 67 is referring to polynucleotides encoding SEQ ID NO:3, 5, 7 and 11 or the polynucleotides encoding the "variants thereof"

9. The following is a quotation of the first paragraph of 35 U.S.C. 112:

> The specification shall contain a written description of the invention, and of the manner and process of making and using it, in such full, clear, concise, and exact terms as to enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make and use the same and shall set forth the best mode contemplated by the inventor of carrying out his invention.

10. Claims 49-52, 54-65, 67, 68, 70-72 and 74-78are rejected under 35 U.S.C. 112, first paragraph, as failing to comply with the written description requirement. The claim(s) contains subject matter which was not described in the specification in such a way as to reasonably

convey to one skilled in the relevant art that the inventor(s), at the time the application was filed, had possession of the claimed invention. .

Claims 49-52 and 54-57 are drawn to polypeptides comprising variants of SEQ ID NO:3, 5 and 7-11 and variants of fragment of SEQ ID NO:3, 5 and 7-11 (see rejection under 112, 2nd, above). Claim 56 is included with this group because it is unclear if said claim is further limiting the fragment or the polypeptide variant of claim 49. Because claim 56 specifies polypeptide "comprising" said polypeptide of the tables, it is reasonable that said short polypeptide of the tables could be comprised within the variant of the polypeptide of claim 49. Claims 63-65, 67, 68 and 78 are drawn to polynucleotide encoding the variant polypeptides of SEQ ID NO:3, 5 and 7-11 and variant fragments of the polypeptides of SEQ ID NO:3, 5 and 7-11. Claims 67 and 68 are included with this group because it is unclear if said claim is further limiting the polynucleotide encoding the fragment or the polynucleotide encoding the polypeptide variant of claim 63. Claim 72 is included in this group because it is dependent on the identity of the genus of polynucleotide encompassed by claim 63.

Claims 58-62, 70, 71 and 75-77 are drawn to method claims reliant upon the identity of the genus of polypeptides of claim 49. Claims 70 and 71 are drawn to method claims reliant upon the identity of the genus of polynucleotide of claim 63.

The specification provides a written description of the polypeptides of SEQ ID NO:3, 5 and 7-11 and peptides consisting of predicted epitopes set forth in Tables VIII-XXI and XXII to XLIX as the HLA Peptide Tables. It is noted that HLA is an acronym for human leukocyte antigen, and differs from the non-human homologues encompassed by major histocompatibility antigen (MHC). The claimed genus of polynucleotide variants encompasses
"a molecule that exhibits a variation from a described type or norm, such as a protein that has one or more different amino acid residues in the corresponding position(s) of a specifically described protein (e.g. the 254P1D6B protein shown in FIG. 2 or FIG. 3. An analog is an example of a variant protein. Splice isoforms and single nucleotides polymorphisms (SNPs) are further examples of variants", and
"allelic variant conservative substitution variants, analogs and homologues that can be isolated/generated and characterized without undue experimentation following the methods outlined herein or readily available in the art".

The specification teaches that SEQ ID NO:3, 5 and 7-11 are related polypeptides which are over-expressed in cancers of the lung, ovary, prostate, pancreas and breast (Table 1, page 122). The specification teaches that SEQ ID NO:3, 5 and 11 differ from each other by only a single nucleotide substitution and SEQ ID NO:7 differs from SEQ ID NO:3 only by a deletion of the first 20amino acids and the substitution of an alternate 10-mer amino acid sequence at the amino terminus (Figure 11). The genus encompassed by "variants" of SEQ ID NO:3, 5, 7 and 11 is highly variant because claim 49 requires only a specific antibody response. Any protein irregardless of function or biological significance can be made to evoke an antibody which binds thereto given the appropriate experimental host and adjuvant. Further, some proteins over-expressed by cancer cells can evoke an endogenous antibody response in the subject having cancer (for example, Sahin et al, PNAS, 1995, Vol. 92, pp. 11810-11813, Scanlan et al, Int Journal of Cancer, 1998, Vol. 76, pp. 652-658 or Cheever et al (U.S. 5,726,023, column 2, lines 50-59). Thus the instant claims drawn to variants, fragments and variants of fragments, are not limited by a functional characteristic of the disclosed SEQ ID NO:3, 5, 7 and 11. The genus encompassed by claims 49, 54, 55 and 57 are not limited in scope to a sequence having any structural relationship to SEQ ID NO:3, 5, 7 and 11 because it appears that the polypeptide of claim 54 can read on a polypeptide having at least 9 contiguous amino acids of the variants of SEQ ID NO:3, 5, 7 and 11 as well as a variant of a fragment having at least 9 contiguous amino acids. Claim 55 also does not impart any structural identity to the variant polypeptides and variant fragments claimed because the presence of an "immuoreactive epitope" is a function of immune recognition in a host, and the claims to not limit the immunoreactivity as being limited to a certain host. Claim 50 encompasses a genus which is also highly variant because there is no limit to the number of substitutions which can be carried out in the conservative variant, and because the resulting variant polypeptide or variant fragment need not share the functional attributes or biological significance of the polypeptides of SEQ ID NO:3, 5, 7 and 11. The disclosure of SEQ ID NO:3, 5, 7 and 11 does not adequately describe the genuses of variant polypeptides claimed because genuses contain members which differ radically in structure and function from SEQ ID NO:3, 5, 7 and 11. The disclosure of the HLA binding peptides in tables VIII to XLIX fails to describe the genus of fragments and variants of fragments which induce a specific antibody response because said genus includes members which do not bind to HLA and

the evoking of the specific antibody response is a function of the host which is not specified by the claim, and further because the variant fragments are not limited by any sequence homology to the disclosed SEQ ID NO:3, 5, 7 and 11. It is noted that the specification contemplates *""254P1D6B-related proteins" of the invention include those specifically identified herein, as well as allelic variant conservative substitution variants, analogs and homologues that can be isolated/generated and characterized without undue experimentation following the methods outlined herein or readily available in the art.* It is recognized in the art that allelic variants arising in nature are due to mutation events and as such cannot be predicted (Glossary of Genetics and Cytogenetics, Reiger et al, Ed.s, 1976, page 17, lines 1-6 of the definition for allele). Further, the contemplation that "variants" includes homologues and analogs which can be isolated, does not confer adequate written description for variants of SEQ ID NO:3, 5, 7 and 11, because one cannot adequately describe that which is at the time of filing unknown.

One of skill in the art would reasonable conclude that applicant was not in possession of the genus of variants and fragments of variants of SEQ ID NO:3, 5, 7 and 11. Claims 65-65, 67, 68, 72 and 78 lack written description because the nucleic acids encoding a genus of polypeptides which are not adequately described cannot be of themselves, adequately described.

Method claims dependent upon the identity of the variant polypeptides or polynucleotide encoding the variant polypeptides cannot be adequately described because the genus on which they depend lacks adequate written description.

11. Claims 70-72 are rejected under 35 U.S.C. 112, first paragraph, as failing to comply with the enablement requirement. The claim(s) contains subject matter which was not described in the specification in such a way as to enable one skilled in the art to which it pertains, or with which it is most nearly connected, to make and/or use the invention..

The factors to be considered in determining whether undue experimentation is required are summarized In re Wands 858 F.2d 731, 8 USPQ2nd 1400 (Fed. Cir, 1988). The court in Wands states: "Enablement is not precluded by the necessity for some experimentation such as routine screening. However, experimentation needed to practice the invention must not be undue experimentation. The key word is 'undue,' not 'experimentation.' " (Wands, 8 USPQ2d 1404). Clearly, enablement of a claimed invention cannot be predicated on the basis of quantity of

experimentation required to make or use the invention. "Whether undue experimentation is needed is not a single, simple factual determination, but rather is a conclusion reached by weighing many factual considerations." (Wands, 8 USPQ2d 1404). The factors to be considered in determining whether undue experimentation is required include: (1) the quantity of experimentation necessary, (2) the amount or direction or guidance presented, (3) the presence or absence of working examples, (4) the nature of the invention, (5) the state of the prior art, (6) the relative skill of those in the art, (7) the predictability or unpredictability of the art, and (8) the breadth of the claims.

(A)As drawn to a method of inhibiting growth, reproduction or survival of cancer cells comprising increasing the amount of cancer antigen in said cells.

Claims 70 and 71 are drawn to a method of inhibiting growth, reproduction or survival of cancer cells that express the polypeptide of claim 49 comprising administering to said cells the polypeptide or polynucleotide encoding said polypeptide, respectively, thereby inhibiting the growth, reproduction or survival of said cells. It is noted that administration to "said cells" requires the administration to the cancer cells, not to the host immune system or to the dendritic cells of a host. The specification teaches that the polypeptides of the instant invention are increased in malignant lung, ovary, prostate, pancreas and breast (Table 1, page 122). A protein which is over-expressed in malignant cells can be looked upon as either merely associated with cancer cells or a causative agent of cancer cells, wherein said causative agent contributes to the malignant phenotype of the cancer cells. In either case, it would not be advantageous to provide the cells with more of the over-expressed protein. It is noted that art teaches that in cases where the over-expressed protein contributes to the phenotype of the malignant cells that either an agent which inhibits the production of said over-expressed protein be administered to inhibit the growth, reproduction of survival of said cancer cells. For example, Gaeta et al (U.S. 5,703,116) teach the inhibition of cancer cells comprising the administration of a compound which inhibits the telomerase activity of a cancer cell (claim 22). Gaeta et al teach that increased telomerase activity contributes to the malignant phenotype pf cancer cells (column 1, line 62 to column 2, line 39). One of skill in the art would reasonable conclude that increasing the level of telomerase in a malignant cell would not contribute to the inhibition of the cancer cell. The art also teaches the targeting of tumor cells expressing over-expressed or uniquely expressed proteins which are

expressed on the cell surface by means of monoclonal antibodies which specifically bind to said protein on the cell surface, wherein the monoclonal antibody serves as a targeting moiety for a toxin or chemotherapeutic agent (Schlom, 'Monoclonal Antibodies: They're More and Less Than You Think', In: Molecular Basis of Clinical Oncology, Broder et al, Ed.s, 1993, pp. 95-133, especially pages 107-109). One of skill in the art would conclude that it would not be efficacious to increase the amount of over-expressed or uniquely expressed protein of a cancer cell by means of administering said protein to the cancer cell, because the art would teach decreasing the protein, or killing the cell which expressed the protein. The specification provides no guidance or objective evidence that uptake of the claimed proteins by cells would inhibit the growth, reproduction or survival of said cells.

(B)As drawn to the administration of proteins in vivo.

Further, the claims encompass a method of administering the polypeptide to cancer cells in vivo by means of treating an individual having a cancer comprising administering polypeptide sequences. In order to fulfill the specific embodiments of the claims the polypeptides would necessary have to contact the cancer cells in vivo. The art recognizes general problems with the administration of protein drugs, namely short half-life in vivo, necessitating multiple administrations (Johnson and Tracey, 'Peptide and Protein Drug Delivery', In: Encyclopedia of Controlled Drug Delivery, Vol. 2, 1999, pages 816-833). The art teaches that "major stability, release and manufacturing challenges" (ibid, page 816, second column, lines 1-5) must be met in order to overcome the technical difficulties associated with the delivery of proteins in vivo. The specification does not teach a means for the delivery of the polypeptide agents to the appropriate site and the efficacious uptake by the tumor to result in the inhibition of cancer cells in a patient. Therefore it would be undue experimentation in order for one of skill in the art to determine the required dosage for the required length of time, and the means to stabilize and then release said polypeptides in vivo using techniques which preserve the ability of said polypeptides to function as claimed.

Given the lack of objective evidence that increasing the amount of polypeptide in claim 49 would inhibit the growth and survival of cancer cells, and the lack of teachings in the specification regarding the amount of polypeptide required and the duration of exposure to the

polypeptide, and the means to provide such, one of skill in the art would be subject to undue experimentation in order to carry out the instant method claims.

(C)As drawn to the administration of polynucleotide in vivo and anti-sense therapy.

Claim 71 is drawn in part to the administration of the polynucleotide encoding the polypeptide of claim 49 and the administration of a polynucleotide complementary to the polynucleotide encoding the polypeptide of claim 49 in a method of inhibiting the growth reproduction or survival of cancer cells that express the polypeptide of claim 49. Claim 72 is drawn to a host cell comprising an expression vector which produces the polypeptides of the instant invention. It is noted that the term "host cell" can read on a cell in an organism which has undergone a gene therapy method, and thus includes a human being. The specification contemplates the delivery of the polynucleotide or the anti-sense polynucleotides as a gene therapy method. The specification is not enabled for either the delivery of the polynucleotide encoding the claims polypeptides or the delivery of anti-sense polynucleotide. The instant specification does not teach how to overcome problems with in vivo delivery and expression with respect to the administration of the claimed nucleic acids or viral vectors comprising said nucleic acids. The state of the art is that in vivo gene delivery is not well developed and is highly unpredictable. For instance Verma et al (Nature, 1997, Vol. 389, pp. 239-242) teach that the Achilles heel of gene therapy is gene delivery. Verma et al state that the ongoing problem is the inability to deliver genes efficiently and to obtain sustained expression (page 239, column 3). Eck et al (Gene-Based Therapy, In: The Pharmacological Basis of Therapeutics, Goodman and Gilman, Ed.s, 1996, pp. 77-101) teach that the fate of the DNA vector itself with regard to the volume of distribution, rate of clearance into tissues etc., the in vivo consequences of altered gene expression and protein function, the fraction of vector taken up by the target cell population, the trafficking of the genetic material within cellular organelles, the rate of degradation of the DNA the level of mRNA produced, the stability of the mRNA produced in vivo, the amount and stability of the protein produced and the proteins compartmentalization or secretory fate within the cell are primary considerations regarding effective therapy. Eck et al state that these factors differ dramatically on the vector used, the protein being produced, and the disease being treated (Eck et al bridging pages 81-82).

As of the priority date sought, it was well known in the art how to infect or transfect cells in vitro or ex vivo with viral vectors. However, using viral vectors to deliver DNA to an organism in vivo, or using infected or transfected cells to deliver nucleic acids which encode a particular protein sequence to an organism in vivo is in the realm of gene therapy, and highly unpredictable in view of the complexity of in vivo systems. Orkin et al ("Report and Recommendation of the Panel to Assess the NIH Investment in Research on Gene Therapy", NIH, 1995) state that clinical efficacy had not been definitively demonstrated with any gene therapy protocol (page 1, second paragraph). Orkin et al defines gene therapy as the transfer of DNA into recipient cells either ex vivo or in vivo (page 7, under the heading "Gene transfer"), thus encompassing the instant claims drawn to the administration of antigen presenting cells transfected or infected ex vivo. Orkin et al concludes that, "none of the available vector systems is entirely satisfactory, and many f the perceived advantages of vector systems have not been experimentally validated. Until progress is made in thee areas, slow and erratic success in applying gene transfer methods to patients can be expected" Orkin et al comment that direct administration of DNA or DNA in liposomes is not well developed and hindered by the low efficiency of gene transfer (page 8, paragraph 5). Orkin et al teach that adequate expression of the transferred genes is essential for therapy, but that the level and consistency of expression of transferred genes in animal models was unknown. Orkin et al states that in protocols not involving ex vivo infections/transfection, it is necessary to target the expression of the transferred genes to the appropriate tissue or cell type by means of regulatory sequences in gene transfer vectors. The specification does not teach a vector having a specific regulatory sequence which would direct the expression of the nucleic acids within the appropriate tissue type.

The specification does not remedy any of the deficiencies or the prior art with regard to the appropriate delivery and expression of an anti-sense construct in a patient. Given the lack of any guidance from the specification on any of the above issues pointed out by Verma or Eck or Orkin. One of skill in the art would be subject to undue experimentation without reasonable expectation of success in order to practice the methods of claims.

When given the broadest reasonable interpretation, claim 71 encompasses anti-sense therapy in vivo. Anti-sense therapy also requires uptake of the administered polynucleotide by the target cells. The specification does not provide dosage or data for administering a

therapeutically effective dosage of the complementary sequences of claim 63 to tumor cells which results in the inhibition of growth, reproduction or survival of cancer cells. It is noted that many anti-sense therapies which appear to be promising using transfection in vitro, fail to provide any therapeutic efficacy when administered in vivo. For instance, Tolcher et al (Clinical Cancer Research, 2002, Vol. 8, pp. 2530-2535) teach that the administration of the anti-sense oligonucleotides ISIS 3521 and 5132 did not possess clinically significant single agent anti-tumor activity in patients having hormone-refractory prostate cancer, although said oligonucleotides were active inhuman tumor models (page 2533, second column, first paragraph under the heading "Discussion"); Cripps et al (Clinical Cancer Research. 2002, 8, pp. 2188-2192) teach that the same oligonucleotides evoked no clinical response in patients having metastatic colorectal cancer. Cripps et al note that although the steady state plasma levels for both oligonucleotide were above the IC50 for inhibition of mRNA expression, these levels may not have been achieved in the target tissue. Cripps et al also contemplate that additional reasons for the lack of efficacy can be that the target RNA was not important for the particular malignancy or that other unknown intracellular event prevented the drugs from effectively inhibiting protein production (page 2191, column 1, bridging paragraph; Marshall et al (Clinical Colorectal Cancer, 2004, Vol. 4, pp. 268-274) teach that the administration of ISIS 3521 to patients having metastatic colorectal cancer produced no tumor response and analysis of tumor biopsies showed minimal uptake of the oligonucleotide in the tumor cells (abstract); Oza et al (Gynecological Oncology, 2003, Vol. 89, pp. 129-133) teach that the administration of the 5132 oligonucleotide to patients with recurrent epithelial ovarian cancer produced no response (page 132, first paragraph under the heading "Discussion"). These reference serve to demonstrate that there is no absolute nexus between the inhibition of tumor cells by administration of anti-sense oligonucleotide in a tumor model or in vitro, with the administration of anti-sense oligonucleotides to a patient with a tumor. The specification fails to address the effect of the anti-sense compound on tumor cell in vitro, therefore it would be a burden placed upon applicant to first attempt to ascertain if the mRNA was important to the cancerous phenotype of the cell as questioned by Cripps et al (ibid). the specification fails to provide a dosage schedule, and the plasma level of the administered oligonucleotides which would be commensurate with the appropriate dosage level at the target tissue, nor does the specification address a specific means

for attaining the appropriate level within the target tissue that would result in the inhibition of the growth and proliferation of the cancer cells. Because of these deficiencies, one of skill in the art would be subject to undue experimentation without reasonable expectation of success in order to practice the claimed invention.

Claim Rejections - 35 USC § 102

12. The following is a quotation of the appropriate paragraphs of 35 U.S.C. 102 that form the basis for the rejections under this section made in this Office action:

> A person shall be entitled to a patent unless –
>
> (a) the invention was known or used by others in this country, or patented or described in a printed publication in this or a foreign country, before the invention thereof by the applicant for a patent.
>
> (b) the invention was patented or described in a printed publication in this or a foreign country or in public use or on sale in this country, more than one year prior to the date of application for patent in the United States.
>
> (e) the invention was described in a patent granted on an application for patent by another filed in the United States before the invention thereof by the applicant for patent, or on an international application by another who has fulfilled the requirements of paragraphs (1), (2), and (4) of section 371(c) of this title before the invention thereof by the applicant for patent.

13. The changes made to 35 U.S.C. 102(e) by the American Inventors Protection Act of 1999 (AIPA) and the Intellectual Property and High Technology Technical Amendments Act of 2002 do not apply when the reference is a U.S. patent resulting directly or indirectly from an international application filed before November 29, 2000. Therefore, the prior art date of the reference is determined under 35 U.S.C. 102(e) prior to the amendment by the AIPA (pre-AIPA 35 U.S.C. 102(e)).

14. Claims 49, 54, 55, 57-61, 63, 67 and 72 are rejected under 35 U.S.C. 102(b) as being anticipated by Cheever et al (U.S. 5,869,445).

Claim 49 is drawn in part to a variant of SEQ ID NO:3, 5, 7 and 11, wherein said variant induces a specific antibody response. Claim 54 embodies the polypeptide of claim 54 wherein the polypeptide consists of at least nine contiguous amino acids. Claim 55 embodies the

polypeptide of claim 49 comprising one or more immuoreactive epitopes. Claim 57 is drawn to a method of generating an immune response in a mammalian subject comprising exposing to cell of the immune system an amount of polypeptide of claim 49 sufficient to generate an immune response. Claim 59 embodies the method of claim 58 wherein the polypeptide has at least one T cell epitope or at least one B cell epitope. Claim 60 embodies the method of claim 59 wherein the immune response comprises an individual cell that generates antibodies that specifically bind to the polypeptide. Claim 61 embodies the method of claim 60 wherein the immune response comprises activating a CTL whereby the CTL kills an autologous cell that expresses the polypeptide. Claim 62 embodies the method of claim 60 wherein the immune [response] comprises activating a T-helper cell, whereby the activated HTL secretes cytokines that facilitate the activity of a cytotoxic CTL or the antibody producing activity of a B cell. Claim 63 is drawn in part to the polynucleotide which encodes the polypeptide of claim 49. Claim 67 embodies the polynucleotide of claim 63 consisting of at least 25 contiguous nucleic acids. Claim 72 is drawn to a host cell modified to contain an expression vector for expressing the polynucleotide of claim 63 and capable of producing the transcribed polypeptide from the polynucleotide.

Cheever et al disclose a method for generating an immune response to a polypeptide comprising administering the cytoplasmic domain of Her-2 (claim 1) in a pharmaceutically acceptable excipient (claim 4). Cheever et al disclose that said polypeptide comprises both a T cell epitope and a B cell epitope (column 17, lines 11-14). Cheever et al disclose the polypeptides, polynucleotides encoding said polypeptide and viral vectors directing the expression of said polypeptides (column 2, lines 25-28 in addition to column 11, lines 57-62). Cheever et al disclose cell transfected ex vivo with the polynucleotide (column 3, lines 5-9) thus fulfilling the specific embodiment of claim 72 drawn to a host cell. Cheever et al disclose the formation of CTL and as part of the immune response to the polypeptide (column 16, lines 62-65). Cheever disclose the CD4+T cell response upon administration of the disclosed polypeptides (column 20, line 66 to column 21. line 22 and column 23, line 25 to column 24, line 17) which fulfills the specific embodiment of claim 62.

The disclosure of Her-2 meets the specific embodiment of a variant of the SEQ ID NO:3, 5, 7 and 11 polypeptides because Her-2 induces a specific antibody response and the rejected

claims do not require and sequence similarity to SEQ ID NO:3, 5, 7 and 11, because there is no limitation restricting the number of amino acid substitutions and additions which can be made

15. Claims 74-77 are rejected under 35 U.S.C. 102(b) as being anticipated by Cheever et al (WO 00/44899).

Claims 74 are drawn to a method of detecting the polynucleotide of claim 63 in a biological sample comprising producing cDNA from said sample and amplification of said cDNA using a second polynucleotide as a primer. Claim 75 is drawn to a method of monitoring expression levels of a polypeptide of claim49 or mRNA encoding said polypeptide in a biological sample from a subject who has or is suspected f having cancer comprising determining the level of the polypeptide of the mRNA expressed by the cells in the sample and comparing said levels to the levels of polypeptide or mRNA in a corresponding normal sample. Claim 76 embodies the method of claim 75 wherein the presence of elevated polypeptide or mRNA relative to the normal sample is indicative of the presence of cancer in the biological sample taken from the subject who has or is suspected of having cancer. Claim 77 embodies the method of claim 76 wherein the cancer occurs in a tissue which is lung or ovary.

Cheever et al disclose that the HER-2/neu gene is over-expressed in a variety of cancers including breast, ovarian, colon, lung and prostate cancer (page 61, lines 29-33). Cheever et al disclose RT-PCR for the detection of Her-2, in which PCR is applied in conjunction with reverse transcription and that a two-fold or greater increase in expression in several dilutions of the test patient sample as compared to the same dilutions of the non-cancerous sample is typically considered positive for cancer (page 67, lines 19-28).

The disclosure of Her-2 meets the specific embodiment of a variant of the SEQ ID NO:3, 5, 7 and 11 polypeptides because Her-2 induces a specific antibody response and the rejected claims do not require and sequence similarity to SEQ ID NO:3, 5, 7 and 11, because there is no limitation restricting the number of amino acid substitutions and additions which can be made.

16. Claims 49 and 51-56 are rejected under 35 U.S.C. 102(e) as being anticipated by Ghosh et al (WO 03/087768, priority to June 17, 2002).

The specific embodiments of the claims are recited above. Gosh et al disclose the polypeptide of Sequence Identifier 1622 which is identical to the instant SEQ ID NO:11 and the polynucleotide encoding said polypeptide. Gosh et al disclose that said polypeptides are human heart mitochondrial proteins.

17. Claims 49, 54 and 55 are rejected under 35 U.S.C. 102(b) as being anticipated by Drmanac et al (WO 01/75067).

Drmanac et al disclose the polypeptide of SEQ ID NO:52425 which consists of residues 1-19 of SEQ ID NO:3,5 and 11. The polypeptide of Drmanac anticipates the current sequences because it has an "X" at the carboxyl terminus encompassing all amino acids. Drmanac et al disclose that polypeptide of the invention can be used to generate an antibody that specifically binds the polypeptide. The polypeptide would thus inherently have at least one immuoreactive epitope.

18. Claims 63, 67 and 68 are rejected under 35 U.S.C. 102(a) as being anticipated by Venter et al (WO 02/68579).

Venter et al disclose the polynucleotide of SEQ ID NO: 12526 which is expressed from the human genome and is a variant of the instant SEQ ID NO:3, 5, 7 and 11 and which would encode a polypeptide that would induce a specific antibody response when administered to an experimental animal.

Claim Rejections - 35 USC § 103

19. The following is a quotation of 35 U.S.C. 103(a) which forms the basis for all obviousness rejections set forth in this Office action:

> (a) A patent may not be obtained though the invention is not identically disclosed or described as set forth in section 102 of this title, if the differences between the subject matter sought to be patented and the prior art are such that the subject matter as a whole would have been obvious at the time the invention was made to a person having ordinary skill in the art to which said subject matter pertains. Patentability shall not be negatived by the manner in which the invention was made.

20. This application currently names joint inventors. In considering patentability of the claims under 35 U.S.C. 103(a), the examiner presumes that the subject matter of the various claims was commonly owned at the time any inventions covered therein were made absent any evidence to the contrary. Applicant is advised of the obligation under 37 CFR 1.56 to point out the inventor and invention dates of each claim that was not commonly owned at the time a later invention was made in order for the examiner to consider the applicability of 35 U.S.C. 103(c) and potential 35 U.S.C. 102(e), (f) or (g) prior art under 35 U.S.C. 103(a).

21. Claim 78 is rejected under 35 U.S.C. 103(a) as being unpatentable over Venter et al (WO 02/68579) in view of Reed et al (WO 02/26780)

Venter et al disclose that double-stranded RNA molecules are useful for, for example, RNA interference, or gene silencing, which can be used to turn genes off in order to elucidate their function (page 16, line 32 to page 17, line 1). Venter et al do not specifically disclose a double stranded RNA which is 19-25 contiguous nucleotides in length.

Reed et al disclose a double stranded RNA fro RNA interference which is 19 contiguous nucleotides in length. Reed et al disclose that double stranded RNA molecules of about 25 nucleotides have also been used for RNA interference (page 49, line 27 to page 50, line 8).

It would have been prima facie obvious at the time the claimed invention was made to make the double stranded RNA from 19-25 contiguous nucleotides of the polynucleotide of SEQ ID NO:12526. One of skill in the art would have been motivated to do so by the teachings of Venter on the use of double stranded RNA to effect gene silencing and the elucidation of gene function.

22. All claims are rejected.

23. Any inquiry concerning this communication or earlier communications from the examiner should be directed to Karen A. Canella whose telephone number is (571)272-0828. The examiner can normally be reached on 11 am to 10 pm, except Wed, Fri.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Larry Helms can be reached on (571)272-0832. The fax phone number for the organization where this application or proceeding is assigned is 571-273-8300.

Information regarding the status of an application may be obtained from the Patent Application Information Retrieval (PAIR) system. Status information for published applications may be obtained from either Private PAIR or Public PAIR. Status information for unpublished applications is available through Private PAIR only. For more information about the PAIR system, see http://pair-direct.uspto.gov. Should you have questions on access to the Private PAIR system, contact the Electronic Business Center (EBC) at 866-217-9197 (toll-free).

Karen A. Canella, Ph.D.
1/23/2006

KAREN A. CANELLA PH.D
PRIMARY EXAMINER

Continuation of Attachment(s) 6). Other: attachment with sequence alignments.

Sequence Alignments – ART Attachment to paper 20060123

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: October 12, 2005, 10:00:24 ; Search time 125 Seconds
(without alignments)
3316.857 Million cell updates/sec

Title: US-10-764-390-3
Perfect score: 5580
Sequence: 1 MAPPTGVLSSLLLLVTIAGC.....VSMNGSIRNGASFSYCSKDR 1072

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	5576	99.9	1072	7	ADJ69816	Adj69816 Human hea
2	5576	99.9	1072	8	ADR00600	Adr00600 Human 254
3	5574	99.9	1072	8	ADR00601	Adr00601 Human 254
4	5574	99.9	1072	8	ADR00597	Adr00597 Human 254
5	5574	99.9	1072	8	ADR00598	Adr00598 Human 254
6	5574	99.9	1072	8	ADR00848	Adr00848 Human 254
7	5574	99.9	1072	8	ADR00594	Adr00594 Human 254
8	5574	99.9	1072	8	ADR00592	Adr00592 Human 254
9	5485	98.3	1053	8	ADR00862	Adr00862 Human 254
10	5485	98.3	1053	8	ADR00863	Adr00863 Human 254
11	5485	98.3	1063	8	ADR00861	Adr00861 Human 254
12	5485	98.3	1063	8	ADR00596	Adr00596 Human 254
13	5485	98.3	1063	8	ADR00599	Adr00599 Human 254
14	4938	88.5	978	7	ADG14994	Adg14994 Human SEC
15	2426.5	43.5	1048	8	ADM36227	Adm36227 Murine SS
16	2401	43.0	1049	4	AAE05768	Aae05768 Human sec
17	2401	43.0	1049	7	ADI21080	Adi21080 Novel hum
18	2086.5	37.4	691	4	AAB95784	Aab95784 Human pro
19	1451.5	26.0	1069	4	ABB63364	Abb63364 Drosophil
20	1440.5	25.8	685	4	AAB94231	Aab94231 Human pro
21	1375	24.6	711	4	ABG08994	Abg08994 Novel hum
22	1296.5	23.2	640	7	ADF42454	Adf42454 Human PP7
23	823	14.7	272	6	ABU70371	Abu70371 Human adi
24	815.5	14.6	346	4	AAM00902	Aam00902 Human bon
25	487	8.7	162	4	AAO09933	Aao09933 Human pol
26	480	8.6	127	5	ADK36703	Adk36703 Novel hum
27	465	8.3	138	2	AAW69431	Aaw69431 Human sec
28	399	7.2	131	5	ADK34788	Adk34788 Novel hum
29	332	5.9	104	5	ABP07182	Abp07182 Human ORF
30	272	4.9	155	3	AAB38389	Aab38389 Human sec
31	232	4.2	1204	6	ABU21703	Abu21703 Protein e
32	225	4.0	34350	8	ADQ89964	Adq89964 Antagonis
33	224	4.0	26926	4	AAU05396	Aau05396 Human tit
34	224	4.0	26926	8	ADQ17316	Adq17316 Human sof
35	222.5	4.0	1946	7	ADC31624	Adc31624 Human nov
36	216	3.9	2402	8	ADO84848	Ado84848 S epiderm
37	213	3.8	7107	4	ABB58144	Abb58144 Drosophil
38	213	3.8	8943	8	ADQ89760	Adq89760 Antagonis
39	212.5	3.8	128	4	AAO07167	Aao07167 Human pol
40	209.5	3.8	5559	6	ABU47253	Abu47253 Protein e
41	208	3.7	5291	7	ADC01014	Adc01014 Enterohae
42	204	3.7	851	3	AAY92718	Aay92718 V. furnis
43	200.5	3.6	31267	6	ABG74786	Abg74786 Human RGS
44	199	3.6	2768	4	ABB68397	Abb68397 Drosophil
45	199	3.6	5701	4	ABB36684	Abb36684 Peptide #

ALIGNMENTS

RESULT 1
ADJ69816
ID ADJ69816 standard; protein; 1072 AA.
XX
AC ADJ69816;
XX
DT 06-MAY-2004 (first entry)
XX
DE Human heat mitochondrial protein as a therapeutic target SeqID1622.
XX
KW mitochondrial; human; screening assay; diabetes mellitus;
KW Huntington's disease; osteoarthritis;
KW Leber's hereditary optic neuropathy; LHON;
KW mitochondrial encephalopathy lactic acidosis and stroke; MELAS;
KW myoclonic epilepsy ragged red fibre syndrome; MERRF; cancer;
KW neuroprotective; nootropic; antidiabetic; anticonvulsant; antiarthritic;
KW osteopathic; ophthalmological; cytostatic.
XX
OS Homo sapiens.
XX
PN WO2003087768-A2.
XX
PD 23-OCT-2003.
XX
PF 04-APR-2003; 2003WO-US010870.
XX
PR 12-APR-2002; 2002US-0372843P.
PR 17-JUN-2002; 2002US-0389987P.
PR 20-SEP-2002; 2002US-0412418P.
XX
PA (MITO-) MITOKOR.
PA (BUCK-) BUCK INST AGE RES.
XX
PI Ghosh SS, Pahy ED, Zhang B, Gibson BW, Taylor SW, Glenn GM;
PI Warnock DE;
XX
DR WPI; 2003-845369/78.
XX
PT Identifying a mitochondrial target for drug screening assays and for
PT treating diseases associated with altered mitochondrial function,
PT comprises detecting a modified polypeptide in a sample and correlating
PT with the disease.
XX
PS Claim 1; SEQ ID NO 1622; 180pp; English.
XX
CC This invention relates to novel mitochondrial targets that can be used
CC for therapeutic intervention in treating a disease associated with
CC altered mitochondrial function. Specifically, it refers to a method for

CC identifying proteins of the human heart mitochondrial proteome that are
CC useful for drug screening assays, as well as therapeutic targets. The
CC present invention describes a method for identifying such proteins that
CC can be used in the treatment of various diseases associated with altered
CC mitochondrial function including diabetes mellitus, Huntington's disease,
CC osteoarthritis, Leber's hereditary optic neuropathy (LHON), mitochondrial
CC encephalopathy lactic acidosis and stroke (MELAS), myoclonic epilepsy
CC ragged red fibre syndrome (MERRF) or cancer. Accordingly, these
CC compositions have neuroprotective, nootropic, antidiabetic,
CC anticonvulsant, antiarthritic, osteopathic, ophthalmological and
CC cytostatic activities. This polypeptide sequence is a human heart
CC mitochondrial protein of the invention.
XX
SQ Sequence 1072 AA;

Query Match 99.9%; Score 5576; DB 7; Length 1072;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1069; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
Qy    1 MAPPTGVLSSLLLLVTIAGCARKQCSEGRTYSNAVISPNLETTRIMRVSHTFPVVDCTAA 60
Db    1 MAPPTGVLSSLLLLVTIAGCARKQCSEGRTYSNAVISPNLETTRIMRVSHTFPVVDCTAA 60

Qy   61 CCDLSSCDLAWWFEGRCYLVSCPHKENCEPKKMGPIRSYLTFVLRPVQRPAQLLDYGDMM 120
Db   61 CCDLSSCDLAWWFEGRCYLVSCPHKENCEPKKMGPIRSYLTFVLRPVQRPAQLLDYGDMM 120

Qy  121 LNRGSPSGIWGDSPEDIRKDLXFLGKDWGLEEMSEYXDDYRELEKDLLQPSGKQEPRGSA 180
Db  121 LNRGSPSGIWGDSPEDIRKDLTFLGKDWGLEEMSEYSDDYRELEKDLLQPSGKQEPRGSA 180

Qy  181 EYTDWGLLPGSEGAFNSSVGDSPAVPAETQQDPELHYLNESASTPAPKLPERSVLLPLPT 240
Db  181 EYTDWGLLPGSEGAFNSSVGDSPAVPAETQQDPELHYLNESASTPAPKLPERSVLLPLPT 240

Qy  241 TPSSGEVLEKEKASQLQEQSSNSSGKEVLMPSHSLPPASLELSSVTVEKSPVLTVTPGST 300
Db  241 TPSSGEVLEKEKASQLQEQSSNSSGKEVLMPSHSLPPASLELSSVTVEKSPVLTVTPGST 300

Qy  301 EHSIPTPPTSAAPSESTPSELPISPTTAPRTVKELTVSAGDNLIITLPDNEVELKAFVAP 360
Db  301 EHSIPTPPTSAAPSESTPSELPISPTTAPRTVKELTVSAGDNLIITLPDNEVELKAFVAP 360

Qy  361 APPVETTYNYEWNLISHPTDYQGEIKQGHKQTLNLSQLSVGLYVFKVTVSSENAFGEGFV 420
Db  361 APPVETTYNYEWNLISHPTDYQGEIKQGHKQTLNLSQLSVGLYVFKVTVSSENAFGEGFV 420

Qy  421 NVTVKPARRVNLPPVAVVSPQLQELTLPLTSALIDGSQSTDDTEIVSYHWEEINGPFIEE 480
Db  421 NVTVKPARRVNLPPVAVVSPQLQELTLPLTSALIDGSQSTDDTEIVSYHWEEINGPFIEE 480

Qy  481 KTSVDSPVLRLSNLDPGNYSFRLTVTDSDGATNSTTAALIVNNAVDYPPVANAGPNHTIT 540
Db  481 KTSVDSPVLRLSNLDPGNYSFRLTVTDSDGATNSTTAALIVNNAVDYPPVANAGPNHTIT 540

Qy  541 LPQNSITLNGNQSSDDHQIVLYEWSLGPGSEGKHVVMQGVQTPYLHLSAMQEGDYTFQLK 600
Db  541 LPQNSITLNGNQSSDDHQIVLYEWSLGPGSEGKHVVMQGVQTPYLHLSAMQEGDYTFQLK 600

Qy  601 VTDSSRQQSTAXVTVIVQPENNRPPVAVAGPDKELIFPVESATLDGSSSSDDHGIVFYHW 660
Db  601 VTDSSRQQSTAVVTVIVQPENNRPPVAVAGPDKELIFPVESATLDGSSSSDDHGIVFYHW 660

Qy  661 EHVRGPSAVEMENIDKAIATVTGLQVGTYHFRLTVKDQQGLSSTSTLTVAVKKENNSPPR 720
Db  661 EHVRGPSAVEMENIDKAIATVTGLQVGTYHFRLTVKDQQGLSSTSTLTVAVKKENNSPPR 720

Qy  721 ARAGGRHVLVLPNNSITLDGSRSTDDQRIVSYLWIRDGQSPAAGDVIDGSDHSVALQLTN 780
Db  721 ARAGGRHVLVLPNNSITLDGSRSTDDQRIVSYLWIRDGQSPAAGDVIDGSDHSVALQLTN 780

Qy  781 LVEGVYTFHLRVTDSQGASDTDTATVEVQPDPRKSGLVELTLQVGVGQLTEQRKDTLVRQ 840
Db  781 LVEGVYTFHLRVTDSQGASDTDTATVEVQPDPRKSGLVELTLQVGVGQLTEQRKDTLVRQ 840

Qy  841 LAVLLNVLDSDIKVQKIRAHSDLSTVIVFYVQSRPPPKVLKAAEVARNLHMRLSKEKADF 900
Db  841 LAVLLNVLDSDIKVQKIRAHSDLSTVIVFYVQSRPPPKVLKAAEVARNLHMRLSKEKADF 900

Qy  901 LLFKVLRVDTAGCLLKCSGHGHCDPLTKRCICSHLWMENLIQRYIWDGESNCEWSIFYVT 960
Db  901 LLFKVLRVDTAGCLLKCSGHGHCDPLTKRCICSHLWMENLIQRYIWDGESNCEWSIFYVT 960

Qy  961 VLAFTLIVLTGGFTWLCICCCKRQKRTKIRKKTKYTILDNMDEQERMELRPKYGIKHRST 1020
Db  961 VLAFTLIVLTGGFTWLCICCCKRQKRTKIRKKTKYTILDNMDEQERMELRPKYGIKHRST 1020

Qy 1021 EHNSSLMVSESEFDSDQDTIPSREKMERGNPKVSMNGSIRNGASFSYCSKDR 1072
Db 1021 EHNSSLMVSESEFDSDQDTIFSREKMERGNPKVSMNGSIRNGASFSYCSKDR 1072
```

RESULT 2
ADR00600
ID ADR00600 standard; protein; 1072 AA.
XX
AC ADR00600;
XX
DT 04-NOV-2004 (first entry)
XX
DE Human 254P1D6B v.5 protein SEQ ID NO:11.
XX
KW 254P1D6B; small interfering RNA; siRNA; immune response;
KW 254P1D6B-related protein; cytostatic; gene therapy; cancer; human;
KW 254P1D6B v.5; chromosome 6.
XX
OS Homo sapiens.
XX
PN WO2004067716-A2.
XX
PD 12-AUG-2004.
XX
PF 23-JAN-2004; 2004WO-US001965.
XX
PR 24-JAN-2003; 2003US-0442526P.
XX
PA (AGEN-) AGENSYS INC.
XX
PI Kanner SB, Raitano AB, Jakobovits A, Challita-Eid PM, Ge W;
PI Perez-Villar JJ, Faris M;
XX
DR WPI; 2004-580991/56.
XX
PT New 254P1D6B siRNA composition comprising a double stranded siRNA that
PT corresponds to the nucleic acid ORF sequence which encodes the 254P1D6B
PT protein or corresponds to a subsequence of the ORF, useful for detecting
PT and treating cancer.
XX
PS Example 1; SEQ ID NO 11; 345pp; English.
XX
CC The present invention describes a 254P1D6B small interfering RNA (siRNA)
CC composition that comprises a double stranded siRNA that corresponds to
CC the nucleic acid open reading frame (ORF) sequence which encodes the
CC 254P1D6B protein, or corresponds to a subsequence of the ORF, where the
CC double stranded siRNA is 19, 20, 21, 22, 23, 24, or 25 contiguous
CC nucleotides in length. Also described: (1) a composition that comprises,
CC consists essentially of, or consists of a peptide of eight, nine, ten, or
CC eleven contiguous amino acids of a protein of figure 2 (P1, see SEQ ID
CC NO:3, 5 or 7 ADR00592, ADR00594 or ADR00596), or a peptide included in
CC any of the 42 lists of peptides, given in the specification, or a protein
CC that is at least 90, 91, 92, 93, 94, 95, 96, 97, 98, or 99% homologous or
CC identical to an entire amino acid sequence of P1; (2) a polynucleotide
CC that encodes the protein; (3) a composition comprising a polynucleotide
CC that is a full complement of the polynucleotide described above; (4)
CC generating a mammalian immune response directed to the protein of P1; (5)
CC detecting, in a sample, the presence of a 254P1D6B-related protein or a

KW 254P1D6B v.2; chromosome 6.
XX
OS Homo sapiens.
XX
PN WO2004067716-A2.
XX
PD 12-AUG-2004.
XX
PF 23-JAN-2004; 2004WO-US001965.
XX
PR 24-JAN-2003; 2003US-0442526P.
XX
PA (AGEN-) AGENSYS INC.
XX
PI Kanner SB, Raitano AB, Jakobovits A, Challita-Eid PM, Ge W;
PI Perez-Villar JJ, Faris M;
XX
DR WPI; 2004-580991/56.
XX
PT New 254P1D6B siRNA composition comprising a double stranded siRNA that
PT corresponds to the nucleic acid ORF sequence which encodes the 254P1D6B
PT protein or corresponds to a subsequence of the ORF, useful for detecting
PT and treating cancer.
XX
PS Example 13; SEQ ID NO 260; 345pp; English.
XX
CC The present invention describes a 254P1D6B small interfering RNA (siRNA)
CC composition that comprises a double stranded siRNA that corresponds to
CC the nucleic acid open reading frame (ORF) sequence which encodes the
CC 254P1D6B protein, or corresponds to a subsequence of the ORF, where the
CC double stranded siRNA is 19, 20, 21, 22, 23, 24, or 25 contiguous
CC nucleotides in length. Also described: (1) a composition that comprises,
CC consists essentially of, or consists of a peptide of eight, nine, ten, or
CC eleven contiguous amino acids of a protein of figure 2 (P1, see SEQ ID
CC NO:3, 5 or 7 ADR00592, ADR00594 or ADR00596), or a peptide included in
CC any of the 42 lists of peptides, given in the specification, or a protein
CC that is at least 90, 91, 92, 93, 94, 95, 96, 97, 98, or 99% homologous or
CC identical to an entire amino acid sequence of P1; (2) a polynucleotide
CC that encodes the protein; (3) a composition comprising a polynucleotide
CC that is a full complement of the polynucleotide described above; (4)
CC generating a mammalian immune response directed to the protein of P1; (5)
CC detecting, in a sample, the presence of a 254P1D6B-related protein or a
CC 254P1D6B-related polynucleotide; (6) a composition that modulates the
CC status of a cell that expresses a protein of P1; (7) a pharmaceutical
CC composition that comprises the composition described above in a human
CC unit dose form; (8) an antibody or its fragment, which is monoclonal; (9)
CC a non-human transgenic animal that produces the antibody; (10) a
CC hybridoma that produces the antibody; (11) delivering a cytotoxic agent
CC or a diagnostic agent to a cell that expresses the protein of P1; and
CC (12) inhibiting growth, reproduction or survival of cancer cells that
CC express the protein of P1. 254P1D6B has cytostatic activity, and can be
CC used in gene therapy. The compositions, molecules and methods are useful
CC for treating and detecting cancer. The present sequence represents a
CC human 254P1D6B v.2 peptide, which is used in the exemplification of the
CC present invention. The human 254P1D6B gene is located on chromosome 6p22.
XX
SQ Sequence 17 AA;

Query Match 1.5%; Score 84; DB 8; Length 17;
Best Local Similarity 94.1%; Pred. No. 24;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 149 GLEEMSEYXDDYRELEK 165
||||||| |||||||
Db 1 GLEEMSEYADDYRELEK 17

RESULT 8
ABG22066
ID ABG22066 standard; protein; 19 AA.
XX
AC ABG22066;
XX
DT 18-FEB-2002 (first entry)
XX
DE Novel human diagnostic protein #22057.
XX
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder.
XX
OS Homo sapiens.
XX
PN WO200175067-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US008631.
XX
PR 31-MAR-2000; 2000US-00540217.
PR 23-AUG-2000; 2000US-00649167.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Drmanac RT, Liu C, Tang YT;
XX
DR WPI; 2001-639362/73.
DR N-PSDB; AAS86253.
XX
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity.
XX
PS Claim 20; SEQ ID NO 52425; 103pp; English.
XX
CC The invention relates to isolated polynucleotide (I) and polypeptide (II)
CC sequences. (I) is useful as hybridisation probes, polymerase chain
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
CC and in recombinant production of (II). The polynucleotides are also used
CC in diagnostics as expressed sequence tags for identifying expressed
CC genes. (I) is useful in gene therapy techniques to restore normal
CC activity of (II) or to treat disease states involving (II). (II) is
CC useful for generating antibodies against it, detecting or quantitating a
CC polypeptide in tissue, as molecular weight markers and as a food
CC supplement. (II) and its binding partners are useful in medical imaging
CC of sites expressing (II). (I) and (II) are useful for treating disorders
CC involving aberrant protein expression or biological activity. The
CC polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic
CC amino acid sequences of the invention. Note: The sequence data for this
CC patent did not appear in the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 19 AA;

Query Match 1.5%; Score 83; DB 4; Length 19;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAPPTGVLSSLLLLVTIA 18
||||||||||||||||||
Db 1 MAPPTGVLSSLLLLVTIA 18

RESULT 9
ADR00854
ID ADR00854 standard; peptide; 24 AA.
XX
AC ADR00854;
XX
DT 04-NOV-2004 (first entry)
XX

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Db       1632 TCAGCCCTGATCGATGGCAGCCAAAGTACAGATGATACTGAAATAGTGAGTTACCACTGG 1691
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Db       1692 GAAGAAGTCGACGGGCCCTTCCTAGGAGAGGAGTTTCCAGCTGACACCCCAATCTTACGA 1751
Qy        491 LeuSerAsnLeuAspProGlyAsnTyrSerPheArgLeuThrValThrAspSerAspGly 510
Db       1752 TTGTCGAACCTAGTTCCTGGTAACTACACCTTTAGGTTGACCATCACAGACTCGGATGGC 1811
Qy        511 AlaThrAsnSerThrThrAlaAlaLeuIleValAsnAsnAlaValAspTyrProProVal 530
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Qy        531 AlaAsnAlaGlyProAsnHisThrIleThrLeuProGlnAsnSerIleThrLeuAsnGly 550
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Qy        551 AsnGlnSerSerAspAspHisGlnIleValLeuTyrGluTrpSerLeuGlyProGlySer 570
Db       1932 AACCAGAGCAGTGATGATCACCAGATTGTTCTCTATGAGTGGTTCGCAGGCCCTGGCGGT 1991
Qy        571 GluGlyLysHisValValMetGlnGlyValGlnThrProTyrLeuHisLeuSerAlaMet 590
Db       1992 GAGAGCAAAGAGATGGTCATGCAGGGAGCGCAGACCCCATACCTTCACTTGTCTGAGCTG 2051
Qy        591 GlnGluGlyAspTyrThrPheGlnLeuLysValThrAspSerSerArgGlnGlnSerThr 610
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Qy        651 AspAspHisGlyIleValPheTyrHisTrpGluHisValArgGlyProSerAlaValGlu 670
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Qy        671 MetGluAsnIleAspLysAlaIleAlaThrValThrGlyLeuGlnValGlyThrTyrHis 690
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Qy        731 LeuProAsnAsnSerIleThrLeuAspGlySerArgSerThrAspAspGlnArgIleVal 750
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Qy        771 AspHisSerValAlaLeuGlnLeuThrAsnLeuValGluGlyValTyrThrPheHisLeu 790
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Db       2652 CTAGTCACTGACAGTCAGGGGGCCTCGGACTCAGACGCGGCCACTGTGGAGGTGCTGCCA 2711
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Db       2832 GACGTGAAGGTGTTGAAGATCCAGGCTCACACGGATGTCAGCACTGTGATTGTATTTTAT 2891
Qy        871 ValGlnSerArgProProPheLysValLeuLysAlaAlaGluValAlaArgAsnLeuHis 890
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Qy        891 MetArgLeuSerLysGluLysAlaAspPheLeuLeuPheLysValLeuArgValAspThr 910
Db       2952 AAGCGGCTTTCCAAGGAGAAGGAGGCTTTCCTGCTTTTCAAGGTCTTGAGGGTAGACACA 3011
Qy        911 AlaGlyCysLeuLeuLysCysSerGlyHisGlyHisCysAspProLeuThrLysArgCys 930
Db       3012 GCAGGGTGCCTTCTCAAGTGTTCAGGCCACGGTCACTGTGACCCCATCACGAAGCGCTGC 3071
Qy        931 IleCysSerHisLeuTrpMetGluAsnLeuIleGlnArgTyrIleTrpAspGlyGluSer 950
Db       3072 ATCTGCTCCCAGCTGTGGATGGAGAACCTCATACAGCGGTACATGTGGGATGGAGAGAGC 3131
Qy        951 AsnCysGluTrpSerIlePheTyrValThrValLeuAlaPheThrLeuIleValLeuThr 970
Db       3132 AACTGTGAGTGGAGTGTATTCTATGTGGCAGCTCTGGCATTGACACTAACACTGCTAACT 3191
Qy        971 GlyGlyPheThrTrpLeuCysIleCysCysCysLysArgGlnLysArgThrLysIleArg 990
Db       3192 GGAGCTGTGTCTTGGCTGTGCATCTGCTGCTGCAGGAGACGGAAAAGGACTAAGATCCGG 3251
Qy        991 LysLysThrLysTyrThrIleLeuAspAsnMetAspGluGlnGluArgMetGluLeuArg 1010
Db       3252 AAGAAAACCAAGTATACCATCCTAGACAGCATGGACGAACAGGAAAGAATGGAACTGAGG 3311
Qy       1011 ProLysTyrGlyIleLysHisArgSerThrGluHisAsnSerSerLeuMetValSerGlu 1030
Db       3312 CCCAAGTACGGTATCAAGCACAGGAGCACGGAGCACAACTCCAGTCTGATGGTGTCGGAG 3371
Qy       1031 SerGluPheAspSerAspGlnAspThrIlePheSerArgGluLysMetGluArgGlyAsn 1050
Db       3372 TCTGAGTTTGAAAGCGACCAGGACACGCTATTCAGCCGAGAGAGGATGGAGAGAGGAGTC 3431
Qy       1051 ProLysValSerMetAsnGlySerIleArgAsnGlyAlaSerPheSerTyrCysSerLys 1070
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Qy       1071 AspArg 1072
Db       3492 GACAGA 3497
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Pg. 3, lines 3-4

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RESULT 3
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LOCUS       CQ726592               2433 bp    DNA     linear   PAT 03-FEB-2004
DEFINITION  Sequence 12526 from Patent WO02068579.
ACCESSION   CQ726592
VERSION     CQ726592.1  GI:42290140
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Venter,C.J., Adams,M.C., Li,P.W. and Myers,E.W.
  TITLE     Kits, such as nucleic acid arrays, comprising a majority of
            humanexons or transcripts, for detecting expression and other uses
            thereof
  JOURNAL   Patent: WO 02068579-A 12526 06-SEP-2002;
            PE Corporation (NY) (US)
FEATURES             Location/Qualifiers
     source          1. .2433
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN

Alignment Scores:

Pred. No.:	8.54e-212	Length:	2433
Score:	4092.00	Matches:	807
Percent Similarity:	80.34%	Conservative:	2
Best Local Similarity:	80.14%	Mismatches:	2
Query Match:	73.33%	Indels:	196
DB:	6	Gaps:	5

US-10-764-390-3 (1-1072) x CQ726592 (1-2433)

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Qy        46 MetArgValSerHisThrProValValAspCysThrAlaAlaCysCysAspLeuSer 65
Db         1 ATGCGGGTGTCTCACACCTTCCCTGTCGTAGACTGCACGGCCGCTTGCTGTGACCTGTCC 60

Qy        66 SerCysAspLeuAlaTrpTrpPheGluGlyArgCysTyrLeuValSerCysProHisLys 85
Db        61 AGCTGTGACCTGGCCTGGTGGTTCGAGGGCCGCTGCTACCTGGTGAGCTGCCCCCACAAA 120

Qy        86 GluAsnCysGluProLysLysMetGlyProIleArgSerTyrLeuThrPheValLeuArg 105
Db       121 GAGAACTGTGAGCCCAAGAAGATGGGCCCCATCAGGTCTTATCTCACTTTTGTGCTCCGG 180

Qy       106 ProValGlnArgProAlaGlnLeuLeuAspTyrGlyAspMetMetLeuAsnArgGlySer 125
Db       181 CCTGTTCAGAGGCCTGCACAGCTGCTGGACTATGGGGACATGATGCTGAACAGGGGCTCC 240

Qy       126 ProSerGlyIleTrpGlyAspSerProGluAspIleArgLysAspLeu***PheLeuGly 145
Db       241 CCCTCGGGGATCTGGGGGGACTCACCTGAGGATATCAGAAAGGACTTGCCCTTTCTAGGC 300

Qy       146 LysAspTrpGlyLeuGluGluMetSerGluTyr***AspAspTyrArgGluLeuGluLys 165
Db       301 AAAGATTGGGGCCTAGAGGAGATGTCTGAGTACTCAGATGACTACCGGGAGCTGGAGAAG 360

Qy       166 AspLeuLeuGlnProSerGlyLysGlnGluProArgGlySerAlaGluTyrThrAspTrp 185
Db       361 GACCTCTTGCAACCCAGTGGCAAGCAGGAGCCCAGAGGGAGTGCCGAGTACACGGACTGG 420

Qy       186 GlyLeuLeuProGlySerGluGlyAlaPheAsnSerSerValGlyAspSerProAlaVal 205
Db       421 GGCCTACTGCCGGGCAGCGAGGGGGCCTTCAACTCCTCTGTTGGAGACAGTCCTGCGGTG 480

Qy       206 ProAlaGluThrGlnGlnAspProGluLeuHisTyrLeuAsnGluSerAlaSerThrPro 225
Db       481 CCAGCGGAGACGCAGCAGGACCCTGAGCTCCATTACCTGAATGAGTCGGCTTCAACCCCT 540

Qy       226 AlaProLysLeuProGluArgSerValLeuLeuProLeuProThrThrProSerSerGly 245
Db       541 GCCCCAAAACTCCCTGAGAGAAGTGTGTTGCTTCCCTTGCCGACTACTCCATCTTCAGGA 600

Qy       246 GluValLeuGluLysGluLysAlaSerGlnLeuGlnGluGlnSerSerAsnSerSerGly 265
Db       601 GAGGTGTTGGAGAAAGAAAAGGCTTCTCAGCTCCAGGAACAATCCAGCAACAGCTCTGGA 660

Qy       266 LysGluValLeuMetProSerHisSerLeuProProAlaSerLeuGluLeuSerSerVal 285
Db       661 AAAGAGGTTCTAATGCCTTCCCATAGTCTTCCTCCGGCAAGCCTGGAGCTCAGCTCAGTC 720

Qy       286 ThrValGluLysSerProValLeuThrValThrProGlySerThrGluHisSerIlePro 305
Db       721 ACCGTGGAGAAAAGCCCAGTGCTCACAGTCACCCCGGGGAGTACAGAGCACAGCATCCCA 780

Qy       306 ThrProProThrSerAlaAlaProSerGluSerThrProSerGluLeuProIleSerPro 325
Db       781 ACACCTCCCACTAGCGCAGCCCCCTCTGAGTCCACCCCATCTGAGCTACCCATATCTCCT 840

Qy       326 ThrThrAlaProArgThrValLysGluLeuThrValSerAlaGlyAspAsnLeuIleIle 345

Db       841 ACCACTGCTCCCAGGACA---------------------------------------- 858

Qy       346 ThrLeuProAspAsnGluValGluLeuLysAlaPheValAlaProAlaProProValGlu 365

Db       859 ----------------------------------------------------------GAA 861

Qy       366 ThrThrTyrAsnTyrGluTrpAsnLeuIleSerHisProThrAspTyrGlnGlyGluIle 385
Db       862 ACAACCTACAACTATGAATGGAATTTAATAAGCCACCCCACAGACTACCAAGGTGAAATA 921

Qy       386 LysGlnGlyHisLysGlnThrLeuAsnLeuSerGlnLeuSerValGlyLeuTyrValPhe 405
Db       922 AAACAAGGACACAAGCAAACTCTTAACCTCTCTCAATTGTCCGTCGGACTTTATGTCTTC 981

Qy       406 LysValThrValSerSerGluAsnAlaPheGlyGluGlyPheValAsnValThrValLys 425
Db       982 AAAGTCACTGTTTCTAGTGAAAACGCCTTTGGAGAAGGATTTGTCAATGTCACTGTTAAG 1041

Qy       426 ProAlaArgArgValAsnLeuProProValAlaValValSerProGlnLeuGlnGluLeu 445

Db      1042 CCT---------------------------------------------------------- 1044

Qy       446 ThrLeuProLeuThrSerAlaLeuIleAspGlySerGlnSerThrAspAspThrGluIle 465

Db      1045 ----------------------------------GAAAGTACAGATGATACTGAAATA 1068

Qy       466 ValSerTyrHisTrpGluGluIleAsnGlyProPheIleGluGluLysThrSerValAsp 485
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Qy       486 SerProValLeuArgLeuSerAsnLeuAspProGlyAsnTyrSerPheArgLeuThrVal 505
Db      1129 TCTCCCGTCTTACGCTTGTCTAACCTTGATCCT---------------------------- 1161

Qy       506 ThrAspSerAspGlyAlaThrAsnSerThrThrAlaAlaLeuIleValAsnAsnAlaVal 525

Db      1162 ----------------------------------GCCCTAATAGTGAACAATGCTGTG 1185

Qy       526 AspTyrProProValAlaAsnAlaGlyProAsnHisThrIleThrLeuProGlnAsnSer 545
Db      1186 GACTACCCACCAGTTGCTAATGCAGGACCAAATCACACCATAACTTTGCCCCAAAACTCC 1245

Qy       546 IleThrLeuAsnGlyAsnGlnSerSerAspAspHisGlnIleValLeuTyrGluTrpSer 565
Db      1246 ATCACTTTGAATGGAAACCAGAGCAGTGACGATCACCAGATTGTCCTCTATGAGTGGTCC 1305

Qy       566 LeuGlyProGlySerGluGlyLysHisValValMetGlnGlyValGlnThrProTyrLeu 585
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Qy       586 HisLeuSerAlaMetGlnGluGlyAspTyrThrPheGlnLeuLysValThrAspSerSer 605
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Qy       606 ArgGlnGlnSerThrAla***ValThrValIleValGlnProGluAsnAsnArgProPro 625

Db      1318 ----------------------------------------AAAAACAATAGACCTCCA 1335

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Qy       646 GlySerSerSerSerAspAspHisGlyIleValPheTyrHisTrpGluHisValArgGly 665
Db      1396 GGGAGCAGCAGCAGCGATGACCACGGCATTGTCTTCTACCACTGGGAGCACGTCAGAGGC 1455

Qy       666 ProSerAlaValGluMetGluAsnIleAspLysAlaIleAlaThrValThrGlyLeuGln 685
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Qy       806 ValGluValGlnProAspProArgLysSerGlyLeuValGluLeuThrLeuGlnValGly 825
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Qy       826 ValGlyGlnLeuThrGluGlnArgLysAspThrLeuValArgGlnLeuAlaValLeuLeu 845
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Qy       846 AsnValLeuAspSerAspIleLysValGlnLysIleArgAlaHisSerAspLeuSerThr 865
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Qy       866 ValIleValPheTyrValGlnSerArgProProPheLysValLeuLysAlaAlaGluVal 885
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Qy       886 AlaArgAsnLeuHisMetArgLeuSerLysGluLysAlaAspPheLeuLeuPheLysVal 905
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ACCESSION   BC028869
VERSION     BC028869.1  GI:20809370
KEYWORDS    MGC.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
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REFERENCE   1  (bases 1 to 4379)
  AUTHORS   Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
            Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
            Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
            Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
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            Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
            Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
            Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
            McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
            Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
            Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
            Fahey,J., Helton,E., Ketteman,M., Madan,A., Rodrigues,S.,
            Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
            Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
            Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
            Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E.,
            Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
  TITLE     Generation and initial analysis of more than 15,000 full-length
            human and mouse cDNA sequences
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
   PUBMED   12477932
REFERENCE   2  (bases 1 to 4379)
  AUTHORS   Strausberg,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (01-MAY-2002) National Institutes of Health, Mammalian
            Gene Collection (MGC), Cancer Genomics Office, National Cancer
            Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
            USA
  REMARK    NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT     Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Jeffrey E. Green, M.D.
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Baylor College of Medicine Human Genome
            Sequencing Center
            Center code: BCM-HGSC
            Web site: http://www.hgsc.bcm.tmc.edu/cdna/
            Contact: amg@bcm.tmc.edu
            Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, H.,
            Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
            A.N., Gibbs, R.A.

            Clone distribution: MGC clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
            Series: IRAK Plate: 37 Row: l Column: 19
            This clone was selected for full length sequencing because it
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                     /tissue_type="Kidney, normal. 5 month old male mouse."
                     /clone_lib="NCI_CGAP_Kid14"
                     /lab_host="DH10B"
                     /note="Vector: pCMV-SPORT6"
```